

REMARKS**Claim Amendments**

Claims 29, 31, 33-34, 37-41, and 43-47 are canceled without prejudice or disclaimer. Claims 25-28, 32 and 35 remain pending. Claim 25 is amended to recite “a method of eliciting a Chlamydia specific immune response in a patient” and “serovar homologue.” No new matter is added by these claim amendments. See, for example, page 9, lines 18-20 of the specification.

Entry of this Amendment is respectfully requested because the response (1) does not raise any new issues, (2) places this application in condition for allowance, and/or (3) simplifies the issues for appeal.

Claim objection

Claim 37 was objected to for a misspelled word. Claims 25 and 37 were objected to for improper Markush claim language. Claim 25 has been amended accordingly. Claim 37 is canceled. Withdrawal of the objection is respectfully requested.

The Rejection of Claims 25-29, 31-35, 37-41, and 43-47 Under 35 U.S.C. § 112, First Paragraph

Claims 25-29, 31-35, 37-41, and 43-47 were rejected under 35 U.S.C. § 112, first paragraph as allegedly failing to provide an adequate written description and enablement. The Office Action asserts that although the specification provides adequate support for the immunogenicity of ribosomal L7/L12, ribosomal L7/L12 protein is allegedly not disclosed as treating or preventing Chlamydia infection. Claims 37-41 and 43-47 have

been canceled. Claim 25 (and dependent claims 26-29 and 31-35), as amended, is directed to a method of eliciting a Chlamydia specific immune response in a patient. The Office Action admits that the specification provides adequate support for eliciting an immune response. Indeed, the specification discloses at page 12, lines 10-12, "seven patients show reactivity to this [ribosomal protein L7/L12] protein, demonstrating that it is immunogenic in humans as a consequence of chlamydial infection" and also discloses at page 8, lines 19-22, "patient immune reactions were also detected against the following proteins: ... spot 12 – ribosomal protein L7/L12 (7/17)". The specification also at page 12, lines 27 to page 13, line 1, discloses "it is noteworthy that several of these new immunoreactive antigens belong to conserved families of bacterial proteins: ... seven sera (41%) recognized [sic] spot 12 (the ribosomal protein L7/L12)."

The Office Action further asserts that the specification allegedly fails to provide an enabling disclosure for a homologue of ribosomal protein L7/L12, a homologue which has greater than 50% identity to ribosomal protein L7/L12, a homologue with greater than 90% identity to ribosomal protein L7/L12 or fragments of ribosomal protein L7/L12 with at least 7 amino acids. Claim 1, as amended, is directed to subject matter which is fully supported by the specification. Therefore, withdrawal of the rejection is respectfully requested.

The specification discloses that the *C. trachomatis* serovar L2 strain was used in obtaining protein samples for immunoblot analysis (page 5, line 28 – page 6, line 3) and the N-terminal sequence data from the proteins was searched in a database for the CT D/UW-3/Cx strain (specification, page 9). The specification further discloses at page 9, lines 17-20 that "although the present study used a *C. trachomatis* serovar L2 strain

(lymphogranuloma biovar), which has a different pathogenicity phenotype, several protein sequences could be safely correlated to the serovar D genes.” Thus, the specification provides a written description of serovar homologues that would enable one of skill in the art to practice the invention without undue experimentation. Withdrawal of the rejection is respectfully requested.

The Rejection of Claims 25-29, 31-35, 37-41, and 43-47 Under 35 U.S.C. § 112, Second Paragraph

Claims 25-29, 31-35, 37-41, and 43-47 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite for recitation of “Chlamydia ribosomal protein L7/L12.” The Office Action asserts that “[i]t appears that ‘L7 and L12’ is a lab[oratory] designation for this protein” and that terminology changes “from lab[oratory] to lab[oratory]”. However, contrary to the Office Action’s assertions, the designation “L7/L12” is recognized in the art. Indeed, the specification discloses ribosomal protein L7/L12 (spot 12) as a known protein (see specification, page 8, lines 22-23). Table 1 from Nature Genetics, Vol. 21, April 1999 is entitled “Functional Assignments of C. Pneumoniae coding sequences; C. trachomatis genes are shown in parentheses.” That table includes the L7/L12 ribosomal protein encoded by the r17 gene (see page 4, col. 2, under the heading “Ribosomal Proteins”). Also, the PubMed status report for Read et al, “Genome Sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39”, *Nucleic Acids Res.*, 28(6), 1397-1406 (2000) describes the 50S ribosomal protein L7/L12. Also, Engel et al, “cloning and Characterization of RNA polymerase core subunits of Chlamydia trachomatis by using the polymerase chain reaction”, *J. Bacteriol.* 172(10), 5732-5741 (1990) describes the L12P family of ribosomal proteins. A reference

previously cited on an Information Disclosure Statement also discusses the L7/L12 proteins (e.g., Sanchez-Campillo et al., *Electrophoresis* 20:2269-2279, 1999). The ribosomal protein L7/L12 is indeed recognized in the art as the specification states. Withdrawal of the rejection is respectfully requested.

Claims 25 and 37 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite under the presumption that "L7/L12" is an abbreviation. As set forth above, "L7/L12" is not an abbreviation. Therefore, withdrawal of the rejection is respectfully requested.

Claims 27, 35, 39, and 47 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite for recitation of "MW of about 15.8 kD." Specifically, the Office Action asserts that the method by which a molecular weight was obtained should be provided. Pointedly, the specification discloses the methods employed in obtaining the molecular weights. For example, the specification at pages 6-7 discloses separation of chlamydial proteins using 2D electrophoresis, immunoblot analysis (Towbin et al (1979) – ref. 18), matching the immunoblot with a reference map and identifying MW and pI coordinates. Claims are not interpreted in a vacuum but rather should be construed in light of the specification (*Ex parte Kotler*, 1901 C.D. 62, 95 O.G. 2684 (Comm'r Pat. 1901). Withdrawal of the rejection is respectfully requested.

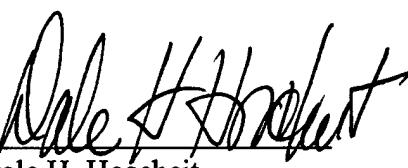
Applicants respectfully submit that the instant application is in condition for allowance. If the Examiner feels, however, that further discussion may be helpful in facilitating prosecution of the case, the Examiner is respectfully requested to telephone the undersigned attorney of record at the number appearing below.

Respectfully submitted,

Dated:

Mar 10, 2004

By:


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Table 1 • Functional assignments of *C. Pneumoniae* coding sequences; *C. trachomatis* genes are shown in parentheses

Amino Acid Biosynthesis			
<i>Aromatic Family</i>			
1039 (CT366) aroA	Phosphoshikimate Vinyltransferase	0871 (CT730) ribD	Riboflavin Deaminase
1036 (CT369) aroB	Dehydroquinate Synthase	0873 (CT732) ribE	Ribityllumazine Synthase
1037 (CT368) aroC	Chorismate Synthase	0320 (CT093) ribF	FAD Synthase
1035 (CT370) aroE	Shikimate 5-Dehydrogenase		
0484 (CT382) aroG	Deoxyheptonate Aldolase		
1038 (CT367) aroL	Shikimate Kinase II		
0740 (CT637) tyrB	Aromatic AA Aminotransferase		
<i>Aspartate Family (lysine)</i>			
1048 (CT363) asd	Aspartate Dehydrogenase	0871 (CT730) ribD	Riboflavin Deaminase
1050 (CT361) dapA	Dihydrodipicolinate Synthase	0873 (CT732) ribE	Ribityllumazine Synthase
1047 (CT364) dapB	Dihydrodipicolinate Reductase	0320 (CT093) ribF	FAD Synthase
0519 (CT430) dapF	Diaminopimelate Epimerase		
1049 (CT362) lysC	Aspartokinase III		
<i>Serine Family</i>			
0433 (CT282) gcsH	Glycine Cleavage System H Protein	0871 (CT730) ribD	Riboflavin Deaminase
0521 (CT432) glyA	Serine Hydroxymethyltransferase	0873 (CT732) ribE	Ribityllumazine Synthase
<i>Base & Nucleotide Metabolism</i>			
0171 guaA	GMP Synthase	0871 (CT730) ribD	Riboflavin Deaminase
0172 guaB	Inosine 5'-Monophosphate Dehydrogenase	0873 (CT732) ribE	Ribityllumazine Synthase
0608	Uridine 5'-Monophosphate Synthase	0320 (CT093) ribF	FAD Synthase
0735	Uridine Kinase		
0244 (CT128) adk	Adenylate Kinase	0871 (CT730) ribD	Riboflavin Deaminase
0894 (CT751) amn	AMP Nucleosidase	0873 (CT732) ribE	Ribityllumazine Synthase
0568 (CT452) cmk	CMP Kinase	0320 (CT093) ribF	FAD Synthase
0392 (CT039) dcd	dCTP Deaminase		
0059 (CT292) dut	dUTP Nucleotidohydrolase		
0120 (CT030) gmk	GMP Kinase		
0619 (CT500) ndk	Nucleoside-2-P Kinase		
0984 (CT827) nrda	Ribonucleoside Reductase, Large Chain		
0985 (CT828) nrdB	Ribonucleoside Reductase, Small Chain		
0236 (CT183) pyrG	CTP Synthetase	0871 (CT730) ribD	Riboflavin Deaminase
0698 (CT678) pyrH	UMP Kinase	0873 (CT732) ribE	Ribityllumazine Synthase
0273 (CT188) tdk	Thymidylate Kinase	0320 (CT093) ribF	FAD Synthase
0659 (CT539) trxA	Thioredoxin		
0314 (CT099) trxR	Thioredoxin Reductase		
1001 (CT844) yfhC	Cytosine Deaminase		
<i>Biosynthesis of Cofactors</i>			
<i>Biotin, Lipoate & Ubiquinone</i>			
1041 bioA	Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase	0871 (CT730) ribD	Riboflavin Deaminase
1044 bioB	Biotin Synthase	0873 (CT732) ribE	Ribityllumazine Synthase
1042 bioD	Dethiobiotin Synthetase	0320 (CT093) ribF	FAD Synthase
0923 (CT777) bioF_1	Oxononanoate Synthase_1		
1043 (CT777) bioF_2	Oxononanoate Synthase_2		
0866 (CT725) birA	Biotin Synthetase		
0748 (CT628) ispA	Geranyl Trantransferase		
0832 (CT558) lipA	Lipoate Synthetase		
0265 (CT219) ubiA	Benzoyl Octaphenyltransferase		
0264 (CT220) ubiD	Phenylacrylate Decarboxylase		
0515 (CT428) ubiE	Ubiquinone Methyltransferase		
<i>Folic Acid</i>			
0759 (CT612) folA	Dihydrofolate Reductase	0871 (CT730) ribD	Riboflavin Deaminase
0335 (CT078) folD	Methylene Tetrahydrofolate Dehydrogenase	0873 (CT732) ribE	Ribityllumazine Synthase
0758 (CT613) folP	Dihydropteroate Synthase	0320 (CT093) ribF	FAD Synthase
0757 (CT614) folX	Dihydronorleotin Aldolase		
0763 (CT649) ygfA	Formyltetrahydrofolate Cycloligase		
<i>Porphyrin</i>			
0714 (CT662) hemA	Glutamyl tRNA Reductase	0871 (CT730) ribD	Riboflavin Deaminase
0744 (CT633) hemB	Porphobilinogen Synthase	0873 (CT732) ribE	Ribityllumazine Synthase
0052 (CT299) hemC	Porphobilinogen Deaminase	0320 (CT093) ribF	FAD Synthase
0890 (CT747) hemE	Uroporphyrinogen Decarboxylase		
0888 (CT745) hemG	protoporphyrinogen Oxidase		
0138 (CT210) hemL	Glutamate-1-Semialdehyde-2,1-Aminomutase		
0380 (CT052) hemN_1	Coproporphyrinogen III Oxidase_1		
0889 (CT746) hemN_2	Coproporphyrinogen III Oxidase_2		
0603 (CT485) hemZ	Ferrochetalase		
<i>Riboflavin</i>			
0872 (CT731) ribA&ribB	GTP Cyclohydrolase & DHBP Synthase	0871 (CT730) ribD	Riboflavin Deaminase
0532 (CT405) ribC	Riboflavin Synthase	0873 (CT732) ribE	Ribityllumazine Synthase
		0320 (CT093) ribF	FAD Synthase
<i>Cell Envelope</i>			
<i>Fatty Acid & Phospholipid Metabolism</i>			
0161 (CT206)	(predicted acyltransferase family)		
0922 (CT776) aas	Acylglycerophosphoethanolamine Acyltransferase		
0414 (CT265) accA	AcCoA Carboxylase/Transferase Alpha		
0183 (CT123) accB	Biotin Carboxyl Carrier Protein		
0182 (CT124) accC	Biotin Carboxylase		
0058 (CT293) accD	AcCoA Carboxylase/Transferase Beta		
0295 (CT236) acpP	Acyl Carrier Protein		
0313 (CT100) acpS	Acyl-carrier Protein Synthase		
0567 (CT451) cdsA	Phosphatidate Cytidylyltransferase		
0297 (CT238) fabD	Malonyl Acyl Carrier Transacylase		
0916 (CT770) fabF	Acyl Carrier Protein Synthase		
0296 (CT237) fabG	Oxoacyl (Carrier Protein) Reductase		
0298 (CT239) fabH	Oxoacyl Carrier Protein Synthase III		
0406 (CT104) fabI	Enoyl-Acyl-Carrier Protein Reductase		
0651 (CT532) fabZ	Myristoyl-Acyl Carrier Dehydratase		
0098 (CT010) htrB	Acyltransferase		
0271 (CT136)	Lysophospholipase Esterase		
0615 (CT496) pgsA_1	Glycerol-3-P Phosphatidyltransferase_1		
0947 (CT797) pgsA_2	Glycerol-3-P Phosphatidyltransferase_2		
0958 (CT807) plsB	Glycerol-3-P Acyltransferase		
0569 (CT453) plsC	Glycerol-3-P Acyltransferase		
0962 (CT811) plsX	FA/Phospholipid Synthesis Protein		
0839 (CT699) psdD	Phosphatidylserine Decarboxylase		
0983 (CT826) pssA	Glycerol-Serine Phosphatidyltransferase		
0921 (CT775)	snGlycerol-3-P Acyltransferase		
0654 (CT535) yciA	Acyl-CoA Thioesterase		
0877 (CT736) ycbL	CT736 Hypothetical Protein		
<i>LPS</i>			
0154 (CT208) gseA	KDO Transferase		
0721 (CT655) kdsA	KDO Synthetase		
0235 (CT182) kdsB	Deoxyoctulonic Acid Synthetase		
0650 (CT531) lpxA	Acyl-Carrier UDP-GlcNAc O-Acyltransferase		
0965 (CT411) lpxB	Lipid A Disaccharide Synthase		
0652 (CT533) lpxC	Myristoyl GlcNAc Deacetylase		
0302 (CT243) lpxD	UDP Glucosamine N-Acyltransferase		
<i>Membrane Proteins, Lipoproteins & Porins</i>			
0310 (CT251) 60IM	60kDa Inner Membrane Protein		
0556 (CT442) crpA	15kDa Cysteine-Rich Protein		
0653 (CT534) cutE	Apolipoprotein N-Acetyltransferase		
0311 (CT252) lgt	Prolipoprotein Diacylglycerol Transferase		
0558 (CT444) omcA	9kDa-Cysteine-Rich Lipoprotein		
0557 (CT443) omcB	60kDa Cysteine-Rich OMP		
0695 (CT681) ompA	Major Outer Membrane Protein		
0854 (CT713) ompB	Outer Membrane Protein B		
0781 (CT600) pal	Peptidoglycan-Associated Lipoprotein		
0300 (CT241) yaeT	Omp85 Homolog		
<i>Peptidoglycan</i>			
0417 (CT268) amiA	N-Acetylmuramoyl Alanine Amidase		
0780 (CT601) amiB	N-Acetylmuramoyl-L-Ala Amidase		
0672 (CT551) dacF	D-Ala-D-Ala Carboxypeptidase		
0968 (CT816) glmS	Glucosamine-Fructose-6-P Aminotransferase		
0749 (CT629) glmU	UDP-GlcNAc Pyrophosphorylase		
0900 (CT757) murA	Muramoyl-Pentapeptide Transferase		
0571 (CT455) murA	UDP-N-Acetylglucosamine Transferase		
0988 (CT831) murB	UDP-N-Acetylglucosaminylpyruvylglucosamine Reductase		
0905 (CT762) murC	Muramoyl-Ala Ligase & D-Ala-D-Alan Ligase		
0901 (CT758) murD	Muramoylalanine-Glutamate Ligase		
0418 (CT269) murE	N-Acetylglucosaminylglutamyl DAP Ligase		
0899 (CT756) murF	Muramoyl-DAP Ligase		
0904 (CT761) murG	Peptidoglycan Transferase		
0902 (CT759) nlpD	Muramidase (invasin repeat family)		
0694 (CT682) pbp2	PBP2-Transglycolase/Transpeptidase		
0419 (CT270) pbp3	Transglycolase/Transpeptidase		
0421 (CT272) yabC	PBP2B Family Methyltransferase		
<i>Cellular Processes</i>			
<i>Cell Division</i>			
0959 (CT808) cafE	Axial Filament Protein		
0880 (CT739) ftsK	Cell Division Protein FtsK		

0903 (CT760)	ftsW	Cell Division Protein FtsW	0202 (CT202)	oppF	Oligopeptide Transport ATPase			
0972 (CT820)	ftsY	Cell Division Protein FtsY	0231 (CT180)	tauB	ABC Transport ATPase (Nitrate/Fe)			
0617 (CT498)	gidA	FAD-dependent Oxidoreductase	0782 (CT599)	tolB	Macromolecule Transporter			
0805 (CT582)	minD	Chromosome Partitioning ATPase	0969 (CT817)	tyrP_1	Tyrosine Transport_1			
0850 (CT709)	mreB	Rod Shape Protein-Sugar Kinase	0970 (CT818)	tyrP_2	Tyrosine Transport_2			
0867 (CT726)	rodA	Rod Shape Protein	0665 (CT544)	uhpC	Hexophosphate Transport			
0684 (CT688)	parB	Chromosome Partitioning Protein	0282 (CT216)	xasA	Amino Acid Transporter			
Detoxification								
0057 (CT294)	sodM	Superoxide Dismutase (Mn)	0207 (CT204)	ybhI	dicarboxylate Translocator			
0778 (CT603)	ahpC	Thio-specific Antioxidant (TSA) Peroxidase	0971 (CT819)	yccA	Transport Permease			
Signal Transduction								
0148 (CT145)		S/T Protein Kinase	0248 (CT152)	ycfV	ABC Transporter ATPase			
0584 (CT467)	atos	Two-Component Sensor	1014 (CT856)	ychM	Sulfate Transporter			
0294 (CT235)		cAMP-Dependent Protein Kinase Regulatory Subunit	0736 (CT641)	ygeD	Efflux Protein			
0712 (CT664)		(FHA domain)	0680 (CT692)	ygoA	Phosphate Permease			
0478 (CT379)	hfIFX	GTP Binding Protein	0723 (CT653)	yhbG	ABC Transporter ATPase			
0703 (CT673)		S/T Protein Kinase	0023 (CT348)	yjjK	ABC Transporter Protein ATPase			
0095 (CT301)		S/T Protein Kinase	0127 (CT034)	ytfF	Cationic Amino Acid Transporter			
0397 (CT259)		PP2C Phosphatase Family	0349 (CT067)	ytgA	Solute Protein Binding Family			
0037 (CT337)	ptsH	PTS Phosphocarrier Protein Hpr	0348 (CT068)	ytgB	ABC transporter ATPase			
0038 (CT336)	ptsI	PTS PEP Phosphotransferase	0347 (CT069)	ytgC	Integral Membrane Protein			
0060 (CT291)	ptsN_1	PTS IIA Protein_1	0346 (CT070)	ytgD	Integral Membrane Protein			
0061 (CT290)	ptsN_2	PTS IIA Protein + HTH DNA-Binding Domain	1012 (CT854)	yzE	ABC Transporter Permease			
0262 (CT218)	surE	SurE-like Acid Phosphatase	0868 (CT727)	zntA	Metal Transport P-type ATPase			
0838 (CT698)	thdF	Thiophene/Furan Oxidation Protein	0279		Possible ABC Transporter Permease Protein			
0693 (CT683)	TPR	Repeats-CT683 Hypothetical Protein	0543 (CT417)		(Metal Transport Protein)			
0321 (CT092)	ychF	GTP Binding Protein	0692 (CT684)		ABC Transporter			
0544 (CT418)	yhbZ	GTP binding protein	0542 (CT416)		ABC Transporter ATPase			
0844 (CT703)	yphC	GTPase/GTP-binding protein	0690 (CT686)		ABC Transporter Membrane Protein			
Standard Protein Secretion								
0115 (CT025)	ffh	Signal Recognition Particle GTPase	0541 (CT415)		solute binding protein			
0363 (CT060)	flhA	Flagellar Secretion Protein	Type-III Secretion					
0858 (CT717)	fliI	Flagellum-specific ATP Synthase	0323 (CT090)	lcrD	Low Calcium Response D			
0704 (CT672)	fliN	Flagellar Motor Switch Domain/YscQ family	0324 (CT089)	lcrE	Low Calcium Response E			
0815 (CT572)	gspD	Gen. Secretion Protein D	0811 (CT576)	lcrH_1	Low Ca Response Protein H_1			
0816 (CT571)	gspE	Gen. Secretion Protein E	1021 (CT862)	lcrH_2	Low Calcium Response_2			
0817 (CT570)	gspF	Gen. Secretion Protein F	0325 (CT088)	syCE	Secretion Chaperone			
0359 (CT064)	lepA	GTPase	0702 (CT674)	yscC	Yop C/Gen Secretion Protein D			
0110 (CT020)	lepB	Signal Peptidase I	0828 (CT559)	yscJ	Yop Translocation J			
0535 (CT408)	ispA	Lipoprotein Signal Peptidase	0826 (CT561)	yscL	Yop Translocation L			
0260 (CT141)	secA_1	Protein Translocase Subunit_1	0707 (CT669)	yscN	Yop N (Flagellar-Type ATPase)			
0841 (CT701)	secA_2	Translocase SecA_2	0825 (CT562)	yscR	Yop Translocation R			
0564 (CT448)	secDsecF	Protein Export Proteins SecD/SecF (fusion)	0824 (CT563)	yscS	YopS Translocation Protein			
0075 (CT321)	secE	Preprotein Translocase	0823 (CT564)	yscT	YopT Tranlocation T			
0629 (CT510)	secY	Translocase	0322 (CT091)	yscU	Yop Translocation Protein U			
0848 (CT707)	tig	Trigger Factor-Peptidyl-prolyl Isomerase	Central Intermediary Metabolism					
Transport-Related Proteins								
0486		Hypothetical Proline Permease	Glycogen Metabolism					
0289 (CT230)	aaaT	Neutral Amino Acid (Glutamate) Transporter	0856 (CT715)		UDP-Glucose Pyrophosphorylase			
0691 (CT685)	abcX	ABC Transporter ATPase	0948 (CT798)	glgA	Glycogen Synthase			
1031 (CT374)	arcD	Arginine/Ornithine Antiporter	0475 (CT866)	glgB	Glucan Branching Enzyme			
0482 (CT381)	artJ	Arginine Periplasmic Binding Protein	0607 (CT489)	glgC	Glucose-1-P Adenyltransferase			
0836 (CT554)	brnQ	Amino Acid (Branched) Transport	0307 (CT248)	glgP	Glycogen Phosphorylase			
0536 (CT409)	daga_1	D-Ala/Gly Permease_1	0388 (CT042)	glgX	Glycogen Hydrolase (debranching)			
0876 (CT735)	daga_2	D-Alanine/Glycine Permease_2	0326 (CT087)	maiQ	Glycanotransferase			
0682 (CT690)	dppD	ABC ATPase Dipeptide Transport	0851 (CT710)	pckA	Phosphoenolpyruvate Carboxykinase			
0683 (CT689)	dppF	ABC ATPase Dipeptide Transport	Phosphorous & Sulfur					
0280 (CT689)	dppF	Dipeptide Transporter ATPase	0548 (CT435)	cysJ	Sulfite Reductase			
0785 (CT596)	exbB	Macromolecule Transporter	0920 (CT774)	cysQ	Sulfite Synthesis/Biphosphate Phosphatase			
0784 (CT597)	exbD	Biopolymer Transport Protein	0025 (CT346)	atsA	Sulphohydrolase			
0604 (CT486)	fliY	Glutamine Binding Protein	0918 (CT772)	ppa	Inorganic Pyrophosphatase			
0192 (CT129)	glnP	ABC Amino Acid Transporter Permease	DNA Replication, Modification, Repair & Recombination					
0191 (CT130)	glnQ	ABC Amino Acid Transporter ATPase	DNA Mismatch Repair					
0528 (CT401)	gitT	Glutamate Symport	0505		3-Methyladenine DNA Glycosylase			
0286 (CT194)	mgte	Mg ⁺⁺ Transporter (CBS Domain)	0812 (CT575)	mutL	DNA Mismatch Repair			
0413 (CT264)	msbA	Transport ATP Binding Protein	0941 (CT792)	mutS	DNA Mismatch Repair			
0290 (CT231)		Na ⁺ -dependent Transporter	0402 (CT107)	mutY	Adenine Glycosylase			
0195 (CT198)	oppA_1	Oligopeptide Binding Protein_1	0732 (CT625)	nfo	Endonuclease IV			
0196 (CT198)	oppA_2	Oligopeptide Binding Protein_2	0837 (CT697)	nth	Endonuclease III			
0197 (CT139)	oppA_3	Oligopeptide Binding Protein_3	DNA Modification					
0198 (CT175)	oppA_4	Oligopeptide Binding Protein_4	0596 (CT477)	ada	Methyltransferase			
0599 (CT480)	oppA_5	Oligopeptide Binding Lipoprotein_5	0114 (CT024)	hemK	A/G-specific Methylase			
0199 (CT199)	oppB_1	Oligopeptide Permease_1	0891 (CT748)	mfd	Transcription-Repair Coupling			
0598 (CT479)	oppB_2	Oligopeptide Permease_2	0620 (CT501)	rvuA	Holliday Junction Helicase			
0200 (CT200)	oppC_1	Oligopeptide Permease_1	0390 (CT040)	rvuB	Holliday Junction Helicase			
0597 (CT478)	oppC_2	Oligopeptide Permease_2	0621 (CT502)	rvuC	Crossover Junction Endonuclease			
0201 (CT201)	oppD	Oligopeptide Transport ATPase	0053 (CT298)	sms	Sms Protein			
			0773 (CT607)	ung	Uracil DNA Glycosylase			
			1062 (CT329)	xseA	Exoxygenribonuclease VII			
DNA Recombination								

0762 (CT650)	recA	RecA Recombination Protein	0160 (CT207)	pfkA_1	Fructose-6-P Phosphotransferase_1
0738 (CT639)	recB	Exodeoxyribonuclease V, Beta	0208 (CT205)	pfkA_2	Fructose-6-P Phosphotransferase_2
0737 (CT640)	recC	Exodeoxyribonuclease V, Gamma	1025 (CT378)	pgi	Glucose-6-P Isomerase
0123 (CT033)	recD_1	Exodeoxyribonuclease V (Alpha Subunit)_1	0679 (CT693)	pgk	Phosphoglycerate Kinase
0752 (CT652)	recD_2	Exodeoxyribonuclease V, Alpha_2	0863 (CT722)	pgmA	Phosphoglycerate Mutase
0339 (CT074)	recF	ABC Superfamily ATPase	0097 (CT332)	pyk	Pyruvate Kinase
0340 (CT074)	(frame-shift with 0339)		1063 (CT328)	tpiS	Triosephosphate Isomerase
0563 (CT447)	recJ	ssDNA Exonuclease	<i>Pentose Phosphate Pathway</i>		
0299 (CT240)	recR	Recombination Protein	0239 (CT186)	devB	Glucose-6-P Dehydrogenase (DevB family)
<i>DNA Replication</i>			1060 (CT331)	dxs	Transketolase
0309 (CT250)	dnaA_1	Replication Initiation Protein_1	0360 (CT063)	gnd	6-Phosphogluconate Dehydrogenase
0424 (CT275)	dnaA_2	Replication Initiation Factor_2	0185 (CT121)	rpe	Ribulose-P Epimerase
0616 (CT497)	dnaB	Replicative DNA Helicase	0141 (CT213)	rplA	Ribose-5-P Isomerase A
0666 (CT545)	dnaE	DNA Pol III Alpha	0083 (CT313)	tal	Transaldolase
0942 (CT794)	dnaG	DNA Primase	0893 (CT750)	tktB	Transketolase
0338 (CT075)	dnaN	DNA Pol III (Beta)	0238 (CT185)	zwf	Glucose-6-P Dehydrogenase
0410 (CT261)	dnaQ_1	DNA Pol III Epsilon Chain_1	<i>Pyruvate Dehydrogenase</i>		
0655 (CT536)	dnaQ_2	DNA Pol III Epsilon Chain_2	0833 (CT557)	lpdA	Lipoamide Dehydrogenase
0040 (CT334)	dnaX_1	DNA Pol III Gamma and Tau_1	0436 (CT285)	lplA_1	Lipoate Protein Ligase-Like Protein
0272 (CT187)	dnaX_2	DNA Pol III Gamma and Tau_2	0618 (CT499)	lplA_2	Lipoate-Protein Ligase A
0149 (CT146)	dnlJ	DNA Ligase	0033 (CT340)	pdhA&B&Oxoisovalerate Dehydrogenase α/β Fusion	
0274 (CT189)	gyrA_1	DNA Gyrase Subunit A_1	0304 (CT245)	pdhA	Pyruvate Dehydrogenase Alpha
0716 (CT660)	gyrA_2	DNA Gyrase Subunit A_2	0305 (CT246)	pdhB	Pyruvate Dehydrogenase Beta
0275 (CT190)	gyrB_1	DNA Gyrase Subunit B_1	0306 (CT247)	pdhC	Dihydrolipoamide Acetyltransferase
0715 (CT661)	gyrB_2	DNA Gyrase Subunit B_2	<i>TCA Cycle</i>		
0416 (CT267)	himD	Integration Host Factor Alpha	0495 (CT390)	aspC	Aspartate Aminotransferase
0612 (CT493)	polA	DNA Polymerase I	1013 (CT855)	fumC	Fumarate Hydratase
0924 (CT778)	priA	Primosomal Protein N'	1028 (CT376)	mdhC	Malate Dehydrogenase
0386 (CT044)	ssb	SS DNA Binding Protein	0789 (CT592)	sdhA	Succinate Dehydrogenase
0835 (CT555)	SWI/SNF family helicase_1		0790 (CT591)	sdhB	Succinate Dehydrogenase
0849 (CT708)	SWI/SNF family helicase_2		0788 (CT593)	sdhC	Succinate Dehydrogenase
0769 (CT643)	topA	DNA Topoisomerase I-Fused to SWI Domain	0378 (CT054)	sucA	Oxoglutarate Dehydrogenase
0024 (CT347)	xerC	Integrase/recombinase	0377 (CT055)	sucB_1	Dihydrolipoamide Succinyltransferase_1
1024 (CT864)	xerD	Integrase/recombinase	0527 (CT400)	sucB_2	Dihydrolipoamide Succinyltransferase_2
<i>Eukaryotic-Type Chromatin Factors</i>			0973 (CT821)	sucC	Succinyl-CoA Synthetase, Beta
0886 (CT743)	hctA	Histone-Like Developmental Protein	0974 (CT822)	sucD	Succinyl-CoA Synthetase, Alpha
0384 (CT046)	hctB	Histone-like Protein 2	<i>Protein Folding, Assembly & Modification</i>		
0878 (CT737)	SET Domain protein		<i>Chaperones</i>		
0577 (CT460)	SWIB (YMT74)	Complex Protein	0949 (CT799)	ctc	General Stress Protein
<i>UVR Exonuclease Repair System</i>			0534 (CT407)	dksA	DnaK Suppressor
0096 (CT333)	uvrA	Excinuclease ABC Subunit A	0032 (CT341)	dnaJ	Heat Shock Protein J
0801 (CT586)	uvrB	Excinuclease ABC Subunit B	0503 (CT396)	dnaK	Hsp-70
0940 (CT791)	uvrC	Excinuclease ABC, Subunit C	0134 (CT110)	groEL_1	Hsp-60_1
0772 (CT608)	uvrD	DNA Helicase	0777 (CT604)	groEL_2	Hsp-60_2
<i>Energy Metabolism</i>			0898 (CT755)	groEL_3	Hsp-60_3
0855 (CT714)	gpdA	Glycerol-3-P Dehydrogenase	0135 (CT111)	groES	10KDa Chaperonin
0743 (CT634)	nqrA	Ubiquinone Oxidoreductase, Alpha	0502 (CT395)	grpE	HSP-70 Cofactor
0427 (CT278)	nqr2	NADH (Ubiquinone) Dehydrogenase	0661 (CT541)	mip	FKBP-type Peptidyl-prolyl Cis-Trans Isomerase
0428 (CT279)	nqr3	NADH (Ubiquinone) Oxidoreductase, Gamma	<i>Proteases</i>		
0429 (CT280)	nqr4	NADH (Ubiquinone) Reductase 4	0144 (CT113)	cipB	Cip Protease ATPase
0430 (CT281)	nqr5	NADH (Ubiquinone) Reductase 5	0437 (CT286)	cipC	CipC Protease
0883 (CT740)	nqr6	Phenolhydrolase/NADH (Ubiquinone) Oxidoreductase 6	0520 (CT431)	cipP_1	CLP Protease
<i>ATP Biogenesis and metabolism</i>			0847 (CT706)	cipP_2	CLP Protease Subunit
0351 (CT065)	adt_1	ADP/ATP Translocase_1	0846 (CT705)	cipX	CLP Protease ATPase
0614 (CT495)	adt_2	ADP/ATP Translocase_2	0269 (CT138)	dipeptidase	Dipeptidase
0088 (CT308)	atpA	ATP Synthase Subunit A	0998 (CT841)	ftsH	ATP-dependent Zinc Protease
0089 (CT307)	atpB	ATP Synthase Subunit B	0030 (CT343)	gcp_1	O-Sialoglycoprotein Endopeptidase_1
0090 (CT306)	atpD	ATP Synthase Subunit D	0194 (CT197)	gcp_2	O-Sialoglycoprotein Endopeptidase_2
0086 (CT310)	atpE	ATP Synthase Subunit E	0979 (CT823)	htrA	DO Serine Protease
0091 (CT305)	atpI	ATP Synthase Subunit I	0957 (CT806)	ide	Insulinase family/Protease III
0092 (CT304)	atpK	ATP Synthase Subunit K	0027 (CT344)	lon	Lon ATP-dependent Protease
0860 (CT719)	fliF	Flagellar M-Ring Protein	1017 (CT859)	lytB	Metalloprotease
<i>Electron Transport Chain</i>			1009 (CT851)	map	Methionine Aminopeptidase
0102 (CT013)	cydA	Cytochrome Oxidase Subunit I	0385 (CT045)	pepA	Leucyl Aminopeptidase A
0103 (CT014)	cydB	Cytochrome Oxidase Subunit II	0136 (CT112)	pepF	Oligopeptidase
0364 (CT059)		Ferredoxin	0813 (CT574)	pepP	Aminopeptidase P
0084 (CT312)		Predicted Ferredoxin	0613 (CT494)	sohB	Protease
<i>Glycolysis & Gluconeogenesis</i>			0555 (CT441)	tsp	Tail-Specific Protease
0281 (CT215)	dhnA	Predicted 1,6-Fructose Biphosphate Aldolase	0344 (CT072)	yaeL	Metalloprotease
0800 (CT587)	eno	Enolase	0981 (CT824)		Zinc Metalloprotease (insulinase family)
0624 (CT505)	gapA	Glyceraldehyde-3-P Dehydrogenase	<i>Protein Isomerases</i>		
0056 (CT295)	mrsA	Phosphomannomutase	0227 (CT176)	dsbB	Disulfide bond Oxidoreductase
0967 (CT815)	pgm	Phosphoglucomutase	0786 (CT595)	dsbD	Thio:disulfide Interchange Protein
			0228 (CT177)	dsbG	Disulfide Bond Chaperone
			0933 (CT783)		Predicted Disulfide Bond Isomerase
			0926 (CT780)		Thioredoxin Disulfide Isomerase

Transcription			Peptide Chain Initiation, Elongation & Termination	
RNA Degradation				
0999 (CT842) pnp	Polyribonucleotide Nucleotidyltransferase	.1067 (CT353) def	Polypeptide Deformylase	
0054 (CT297) rnc	Ribonuclease III	0184 (CT122) efp_1	Elongation Factor P_1	
0119 (CT029) rnhB_1	Ribonuclease HII_1	0895 (CT752) efp_2	Elongation Factor P_2	
1068 (CT008) rnhB_2	Ribonuclease HII_2	0550 (CT437) fusA	Elongation Factor G	
0934 (CT784) rnpA	Ribonuclease P Protein Component	0073 (CT323) infA	Initiation Factor IF-1	
0504 (CT397) vacB	Ribonuclease Family	0317 (CT096) infB	Initiation Factor-2	
RNA Elongation & Termination Factors			0990 (CT833) infC	Initiation Factor 3
0741 (CT636) greA	Transcription Elongation Factor	0113 (CT023) pfrA	Peptide Chain Releasing Factor 1	
0316 (CT097) nusA	N Utilization Protein A	0576 (CT459) prfB	Peptide Chain Release Factor 2	
0076 (CT320) nusG	Transcriptional Antitermination	0950 (CT800) pth	Peptidyl tRNA Hydrolase	
0845 (CT704) pcnB_1	Poly A Polymerase_1	0318 (CT095) rbfA	Ribosome Binding Factor A	
0966 (CT410) pcnB_2	PolyA Polymerase_2	0699 (CT677) rrf	Ribosome Releasing Factor	
0610 (CT491) rho	Transcription Termination Factor	0697 (CT679) tsf	Elongation Factor TS	
RNA Methylases			0074 (CT322) tufA	Elongation Factor Tu
0674 (CT553) fmu	RNA Methyltransferase	Ribosomal Proteins		
1059 (CT354) kgsA	Dimethyladenosine Transferase	0078 (CT318) rl1	L1 Ribosomal Protein	
0187 (CT133) Predicted Methylase		0644 (CT525) rl2	L2 Ribosomal Protein	
0530 (CT403) spou_1	rRNA Methylase_1	0647 (CT528) rl3	L3 Ribosomal Protein	
0660 (CT540) spou_2	rRNA Methylase_2	0646 (CT527) rl4	L4 Ribosomal Protein	
0117 (CT027) trmD	tRNA (Guanine N-1)-Methyltransferase	0635 (CT516) rl5	L5 Ribosomal Protein	
0885 (CT742) ygca	rRNA Methyltransferse	0633 (CT514) rl6	L6 Ribosomal Protein	
0986 (CT829) yggH	Predicted rRNA Methylase	0080 (CT316) rl7	L7/L12 Ribosomal Protein	
0987 (CT830) ytgB	Predicted rRNA Methylase	0953 (CT803) rl9	L9 Ribosomal Protein	
RNA Modification			0079 (CT317) rl10	L10 Ribosomal Protein
0649 (CT530) fmt	Methionyl tRNA Formyltransferase	0077 (CT319) rl11	L11 Ribosomal Protein	
0910 (CT766) miaA	tRNA Pyrophosphate Transferase	0247 (CT125) rl13	L13 Ribosomal Protein	
0719 (CT658) sfhB	Predicted Pseudouridine Synthase	0637 (CT518) rl14	L14 Ribosomal Protein	
0219 (CT193) tgt	Queuine tRNA Ribosyl Transferase	0630 (CT511) rl15	L15 Ribosomal Protein	
0580 (CT463) truA	Pseudouridylate Synthase I	0640 (CT521) rl16	L16 Ribosomal Protein	
0319 (CT094) truB	tRNA Pseudouridine Synthase	0625 (CT506) rl17	L17 Ribosomal Protein	
0403 (CT106) yecC	Predicted Pseudouridine Synthetase Family	0632 (CT513) rl18	L18 Ribosomal Protein	
0864 (CT723) yjbC	Predicted Pseudouridine Synthase	0118 (CT028) rl19	L19 Ribosomal Protein	
RNA Polymerase & Transcription Regulators			0992 (CT835) rl20	L20 Ribosomal Protein
0586 (CT468) atoC	Two-Component Regulator	0546 (CT420) rl21	L21 Ribosomal Protein	
0362 (CT061) rpsD	Sigma-28/WhiG Family	0642 (CT523) rl22	L22 Ribosomal Protein	
0501 (CT394) hrcA	HTH Transcriptional Repressor	0645 (CT526) rl23	L23 Ribosomal Protein	
0793 (CT588) rbsU	Sigma Regulatory Family Protein—PP2C Phosphatase (RsbW Antagonist)	0636 (CT517) rl24	L24 Ribosomal Protein	
0626 (CT507) rpoA	RNA Polymerase Alpha	0545 (CT419) rl27	L27 ribosomal protein	
0081 (CT315) rpoB	RNA Polymerase Beta	0327 (CT086) rl28	L28 Ribosomal Protein	
0082 (CT314) rpoC	RNA Polymerase Beta'	0639 (CT520) rl29	L29 Ribosomal Protein	
0756 (CT615) rpoD	RNA Polymerase Sigma-66	0112 (CT022) rl31	L31 Ribosomal Protein	
0771 (CT609) rpoN	RNA Polymerase Sigma-54	0961 (CT810) rl32	L32 Ribosomal Protein	
0511 (CT424) rsvV_1	Sigma Regulatory Factor_1	0250 (CT150) rl33	L33 Ribosomal Protein	
0909 (CT765) rsvV_2	Sigma Factor Regulator_2	0935 (CT785) rl34	L34 Ribosomal Protein	
0670 (CT549) rsvW	Sigma Regulatory Factor-Histidine Kinase	0991 (CT834) rl35	L35 Ribosomal Protein	
0750 (CT630) tctD	HTH Transcriptional Regulatory Protein + Receiver Doman	0936 (CT786) rl36	L36 Ribosomal Protein	
1069 (CT009) yfgA	HTH Transcriptional Regulator	0315 (CT098) rs1	S1 Ribosomal Protein	
Translation			0696 (CT680) rs2	S2 Ribosomal Protein
Amino Acyl tRNA Synthesis			0641 (CT522) rs3	S3 Ribosomal Protein
0892 (CT749) alaS	Alanyl tRNA Synthetase	0733 (CT626) rs4	S4 Ribosomal Protein	
0570 (CT454) argS	Arginyl tRNA Transferase	0631 (CT512) rs5	S5 Ribosomal Protein	
0662 (CT542) aspS	Aspartyl tRNA Synthetase	0951 (CT801) rs6	S6 Ribosomal Protein	
0932 (CT782) cysS	Cysteinylin tRNA Synthetase	0551 (CT438) rs7	S7 Ribosomal Protein	
0003 (CT003) gatA	Glu tRNA Gln Amidotransferase (A subunit)	0634 (CT515) rs8	S8 Ribosomal Protein	
0004 (CT004) gatB	Glu tRNA Gln Amidotransferase (B Subunit)	0246 (CT126) rs9	S9 Ribosomal Protein	
0002 (CT002) gatC	Glu tRNA Gln Amidotransferase (C subunit)	0549 (CT436) rs10	S10 Ribosomal Protein	
0560 (CT445) gltX	Glutamyl-tRNA Synthetase	0627 (CT508) rs11	S11 Ribosomal Protein	
0946 (CT796) glyQ	Glycyl tRNA Synthetase	0552 (CT439) rs12	S12 Ribosomal Protein	
0663 (CT543) hisS	Histidyl tRNA Synthetase	0628 (CT509) rs13	S13 Ribosomal Protein	
0109 (CT019) ileS	Isoleucyl-tRNA Synthetase	0937 (CT787) rs14	S14 Ribosomal Protein	
0153 (CT209) leuS	Leucyl tRNA Synthetase	1000 (CT843) rs15	S15 Ribosomal Protein	
0931 (CT781) lysS	Lysyl tRNA Synthetase	0116 (CT026) rs16	S16 Ribosomal Protein	
0122 (CT032) metG	Methionyl-tRNA Synthetase	0638 (CT519) rs17	S17 Ribosomal Protein	
0993 (CT836) phes	Phenylalanyl tRNA Synthetase, Alpha	0952 (CT802) rs18	S18 Ribosomal Protein	
0594 (CT475) pheT	Phenylalanyl tRNA Synthetase Beta	0643 (CT524) rs19	S19 Ribosomal Protein	
0500 (CT393) proS	Prolyl tRNA Synthetase	0754 (CT617) rs20	S20 Ribosomal Protein	
0870 (CT729) serS	Seryl tRNA Synthetase_2	0031 (CT342) rs21	S21 Ribosomal Protein	
0806 (CT581) thrS	Threonyl tRNA Synthetase	Other Categories		
0802 (CT585) trpS	Tryptophanyl tRNA Synthetase	Chlamydia-Specific Proteins		
0361 (CT062) tyrS	Tyrosyl tRNA Synthetase	0561 (CT446) Euo	CHLPS Euo Protein	
0094 (CT302) valS	Valyl tRNA Synthetase	0804 (CT583) Gp6D	CHLTR Plasmid Paralog	
		0186 (CT119)	Similarity to Inca_1	
		0291 (CT232) incB	Inclusion Membrane Protein B	
		0292 (CT233) incC	Inclusion Membrane Protein C	
		1026 (CT377)	LtuA Protein	
		0333 (CT080)	LtuB Protein	
		0005 (CT871) pmp_1	Polymorphic Outer Membrane Protein G Family	

0013 (CT871)	pmp_2	Polymorphic Outer Membrane Protein G Family	0734 (CT627)	yceA	YceA Hypothetical Protein
0014 (CT871)	pmp_3	Polymorphic Outer Membrane Protein G Family	0954 (CT804)	ychB	Predicted Kinase
0015 (CT871)	pmp_3	PMP_3 (frame-shift with 0014)	0261 (CT217)	ydaO	PP-Loop Superfamily ATPase
0016 (CT874)	pmp_4	Polymorphic Outer Membrane Protein G Family	0245 (CT127)	ydhO	Polysaccharide Hydrolase-Invasin Repeat Family
0017 (CT871)	pmp_4	PMP_4 (frame-shift with 0016)	0573 (CT457)	yebC	YebC Family Hypothetical Protein
0018 (CT874)	pmp_5	Polymorphic Outer Membrane Protein G Family	0689 (CT687)	yfhO_1	NifS-related Aminotransferase_1
0019 (CT871)	pmp_5	PMP_5 (frame-shift with 0018)	0862 (CT721)	yfhO_2	NifS-related Aminotransferase_2
0444 (CT871)	pmp_6	Polymorphic Outer Membrane Protein G/I Family	0547 (CT434)	ygbB	YgbB Family Hypothetical Protein
0445 (CT871)	pmp_7	Polymorphic Outer Membrane Protein G Family	0237 (CT184)	yggF	YggF Family Hypothetical Protein
0446 (CT871)	pmp_8	Polymorphic Outer Membrane Protein G Family	0775 (CT606)	yggV	YggV Family Hypothetical Protein
0447 (CT871)	pmp_9	Polymorphic Outer Membrane Protein G/I Family	0396 (CT258)	yhfO_3	NifS-related Aminotransferase_3
0450 (CT871)	pmp_10	Polymorphic Outer Membrane Protein G Family	0605 (CT487)	yhhF	Predicted Methylase
0449 (CT871)	pmp_10	PMP_10 (Frame-shift with 0450)	0575 (CT458)	yhhY	Amino Group Acetyl Transferase
0451 (CT871)	pmp_11	Polymorphic Outer Membrane Protein G Family	0592 (CT473)	yidD	YidD Family
0452 (CT874)	pmp_12	Polymorphic Outer Membrane Protein (truncated) A/I Family	0982 (CT825)	yigN	YigN Family Hypothetical Protein
0453 (CT871)	pmp_13	Polymorphic Outer Membrane Protein G Family	0657 (CT537)	yjeE	YjeE Hypothetical Protein
0454 (CT872)	pmp_14	Polymorphic Outer Membrane Protein H Family	0768 (CT644)	yohI	YohI Predicted Oxidoreductase
0466 (CT869)	pmp_15	Polymorphic Outer Membrane Protein E Family	0336 (CT077)	yolJ	YolJ Hypothetical Protein
0467 (CT869)	pmp_16	Polymorphic Outer Membrane Protein E Family	0217 (CT140)	ypdP	YpdP Hypothetical Protein
0468 (CT869)	pmp_17	Polymorphic Outer Membrane Protein E Family	0140 (CT212)	yqdE	YqdE Hypothetical Protein
0469 (CT869)	pmp_17	PMP_17 (Frame-shift with 0468)	0263 (CT221)	yqfU	YqfU Hypothetical Protein
0470 (CT869)	pmp_17	PMP_17 (Frame-shift with 0469)	0139 (CT211)	yqeE	YqeE Hypothetical Protein
0471 (CT870)	pmp_18	Polymorphic Outer Membrane Protein E/F Family	0270 (CT137)	ywlC	SuAS Superfamily-related Protein
0539 (CT412)	pmp_19	Polymorphic Membrane Protein A Family	0879 (CT738)	yycJ	Metal Dependent Hydrolase
0540 (CT413)	pmp_20	Polymorphic Membrane Protein B Family			
0963 (CT812)	pmp_21	Polymorphic Membrane Protein D Family			
0562		CHLPS 43 kDa Protein Homolog_1			
0927		CHLPS 43 kDa Protein Homolog_2			
0928		CHLPS 43 kDa Protein Homolog_3			
0929		CHLPS 43 kDa Protein Homolog_4			
0728 (CT622)		CHLPN 76kDa Homolog_1 (CT622)			
0729 (CT623)		CHLPN 76kDa Homolog_2 (CT623)			
0133 (CT109)		CHLPS Hypothetical Protein			
0332 (CT081)		CHLTR T2 Protein			
Miscellaneous Enzymes/Conserved Proteins					
0193	argR	Possible Arginine Repressor	0001 (CT001)	CT001	Hypothetical Protein
1046		Aromatic Amino Acid Hydroxylase	0020 (CT351)	CT351	Hypothetical Protein
0232		Similarity to 5'-Methylthioadenosine Nucleosidase	0021 (CT350)	CT350	Hypothetical Protein
0128 (CT035)		Biotin Protein Ligase	0026 (CT345)	CT345	Hypothetical Protein
0513 (CT426)		Fe-S Oxidoreductase_1	0035 (CT339)	CT339	Hypothetical Protein
0911 (CT767)		Fe-S Oxidoreductase_2	0036 (CT338)	CT338	Hypothetical Protein
0373 (CT057)	gcPE	GcpE Protein	0055 (CT296)	CT296	Hypothetical Protein
0407 (CT103)		HAD Superfamily Hydrolase/Phosphatase	0062 (CT289)	CT289	Hypothetical Protein
0917 (CT771)		Hydrolase/Phosphatase Homolog	0065 (CT288)	CT288	Hypothetical Protein
0488 (CT385)	ycfF	HIT Family Hydrolase	0068 (CT360)	CT360	Hypothetical Protein
0701 (CT675)	karg	Arginine Kinase	0071 (CT325)	CT325	Hypothetical Protein
0526 (CT399)	kpsF	GutQ/KpsF Family Sugar-P Isomerase	0072 (CT324)	CT324	Hypothetical Protein
0919 (CT773)	ldh	Leucine Dehydrogenase	0085 (CT311)	CT311	Hypothetical Protein
0022 (CT349)	maf	Maf protein	0087 (CT309)	CT309	Hypothetical Protein
0997 (CT840)	mesJ	PP-loop superfamily ATPase	0093 (CT303)	CT303	Hypothetical Protein
0151 (CT148)	mhpA	Monooxygenase	0100 (CT011)	CT011	Hypothetical Protein
0730 (CT624)	mvnN	Integral Membrane Protein	0104 (CT017)	CT017	Hypothetical Protein
0861 (CT720)		NifU-Related Protein	0105 (CT016)	CT016	Hypothetical Protein
0479 (CT380)	phnP	Metal Dependent Hydrolase	0107 (CT058)	CT058	Hypothetical Protein_1
0106 (CT015)	phoH	ATPase	0108 (CT018)	CT018	Similarity
0329 (CT084)		Phopholipase D Superfamily	0111 (CT021)	CT021	Hypothetical Protein
0435 (CT284)		Phospholipase D Superfamily	0121 (CT031)	CT031	Hypothetical Protein
0581 (CT464)		Phosphoglycolate Phosphatase	0129 (CT036)	CT036	Similarity
0897 (CT754)		Predicted Phosphohydrolase	0145 (CT114)	CT114	Hypothetical Protein
0509 (CT422)		Predicted Metalloenzyme	0150 (CT147)	CT147	Hypothetical Protein
1030 (CT375)		Predicted D-Amino Acid Dehydrogenase	0152 (CT149)	CT149	Hypothetical Protein
0531 (CT404)		SAM Dependent Methyltransferase	0176 (CT153)	CT153	Hypothetical Protein
0337 (CT076)	smpB	Small Protein B	0188 (CT132)	CT132	Hypothetical Protein
0394 (CT256)	tlyC_1	CBS Domain Protein (Hemolysin Homolog)_1	0189 (CT131)	CT131	Hypothetical Protein
0510 (CT423)	tlyC_2	CBS Domains (Hemolysin Homolog)_2	0206 (CT203)	CT203	Hypothetical Protein
0382 (CT048)	yabc	SAM-Dependent Methytransferase	0229 (CT178)	CT178	Hypothetical Protein
0787 (CT594)	yabd	PHP Superfamily (Urease/Pyrimidinase) Hydrolase	0230 (CT179)	CT179	Hypothetical Protein
0611 (CT492)	yacE	Predicted Phosphatase/Kinase	0234 (CT181)	CT181	Hypothetical Protein
0579 (CT462)	yacM	Sugar Nucleotide Phosphorylase	0249 (CT151)	CT151	Hypothetical Protein
0578 (CT461)	yael	Phosphohydrolase	0253 (CT144)	CT144	Hypothetical Protein_1
0345 (CT071)	yaeM	CT071 Hypothetical Protein	0254 (CT143)	CT143	Hypothetical Protein_1
0566 (CT450)	yaes	YaeS family Hypothetical Protein	0255 (CT142)	CT142	Hypothetical Protein_1
0591 (CT472)	yage	YagE family	0256 (CT144)	CT144	Hypothetical Protein_2
0039 (CT335)	ybab	YbaB family Hypothetical Protein	0257 (CT143)	CT143	Hypothetical Protein_2
0101 (CT012)	ybbP	YbbP family Hypothetical Protein	0259 (CT142)	CT142	Hypothetical Protein_2
0915 (CT769)	ybeb	iojap Superfamily Ortholog	0276 (CT191)	CT191	Hypothetical Protein
0137 (CT108)	ybgl	ACR family	0288 (CT195)	CT195	Hypothetical Protein
0529 (CT402)	ycaH	ATPase	0293 (CT234)	CT234	Hypothetical Protein
0438 (CT287)	ycbf	PP-loop Superfamily ATPase	0301 (CT242)	CT368	Hypothetical Protein
			0303 (CT244)	CT244	Hypothetical Protein
			0308 (CT249)	CT249	Similarity
			0312 (CT101)	CT101	Hypothetical Protein
			0328 (CT085)	CT085	Hypothetical Protein
			0330 (CT083)	CT083	Hypothetical Protein
			0331 (CT082)	CT082	Hypothetical Protein
			0334 (CT079)	CT079	Similarity
			0342 (CT073)	CT073	Hypothetical Protein
			0343 (CT073)	(frame-shift with 0342?)	
			0350 (CT066)	CT066	Hypothetical Protein
			0369 (CT058)	CT058	Hypothetical Protein_2

0370 (CT058)	CT058 Hypothetical Protein_3
0374 (CT056)	CT056 Hypothetical Protein
0379 (CT053)	CT053 Hypothetical Protein
0381 (CT326)	CT326 Similarity
0383 (CT047)	CT047 Hypothetical Protein
0387 (CT043)	CT043 Hypothetical Protein
0389 (CT041)	CT041 Hypothetical Protein
0393 (CT038)	CT038 Hypothetical Protein
0395 (CT257)	CT257 Hypothetical Protein
0399 (CT253)	CT253 Hypothetical Protein
0400 (CT254)	CT254 Hypothetical Protein
0401 (CT255)	CT255 Hypothetical Protein
0405 (CT105)	CT105 Hypothetical Protein
0408 (CT102)	CT102 Hypothetical Protein
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0412 (CT263)	CT263 Hypothetical Protein
0415 (CT266)	CT266 Hypothetical Protein
0420 (CT271)	CT271 Hypothetical Protein
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0425 (CT276)	CT276 Hypothetical Proteins
0426 (CT277)	CT277 Similarity
0434 (CT283)	CT283 Hypothetical Protein
0441 (CT007)	CT007 Hypothetical Protein
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0443 (CT005)	CT005 Hypothetical Protein
0474 (CT365)	CT365 Hypothetical Protein
0476 (CT865)	CT865 Hypothetical Protein
0480 (CT383)	CT383 Hypothetical Protein
0485 (CT382)	CT382.1 Hypothetical Protein
0487 (CT384)	CT384 Hypothetical Protein
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0491 (CT389)	CT389 Hypothetical Protein
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0497 (CT388)	CT388 Hypothetical Protein
0506 (CT421)	CT421 Hypothetical Protein
0507 (CT421)	CT421.1 Hypothetical Protein
0508 (CT421)	CT421.2 Hypothetical Protein
0512 (CT425)	CT425 Hypothetical Protein
0514 (CT427)	CT427 Hypothetical Protein
0518 (CT429)	CT429 Hypothetical Protein
0522 (CT433)	CT433 Hypothetical Protein
0525 (CT398)	CT398 Hypothetical Protein
0533 (CT406)	CT406 Hypothetical Protein
0537 (CT814)	CT814.1 Hypothetical Protein
0538 (CT814)	CT814 Hypothetical Protein
0554 (CT440)	CT440 Hypothetical Protein
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0565 (CT449)	CT449 Hypothetical Protein
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0622 (CT503)	CT503 Hypothetical Protein
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0676 (CT695)	CT695 Similarity
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0725 (CT652)	CT652.1 Hypothetical Protein
0726 (CT620)	CT620 Hypothetical Protein
0727 (CT619)	CT619 Hypothetical Protein
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0746 (CT632)	CT632 Hypothetical Protein
0747 (CT631)	CT631 Hypothetical Protein
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0770 (CT642)	CT642 Hypothetical Protein
0774 (CT606)	CT606.1 Hypothetical Protein
0776 (CT605)	CT605 Hypothetical Protein
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0884 (CT741)	CT741 Hypothetical Protein
0887 (CT744)	CHLTR Possible Phosphoprotein
0896 (CT753)	CT753 Hypothetical Protein
0906 (CT763)	CT763 Hypothetical Protein
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0996 (CT839)	CT839 Hypothetical Protein
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1004 (CT847)	CT847 Hypothetical Protein
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1007 (CT849)	CT849.1 Hypothetical Protein
1008 (CT850)	CT850 Hypothetical Protein
1010 (CT852)	CT852 Hypothetical Protein

1011	(CT853)	CT853 Hypothetical Protein	0011	0205	0459	1029
1015	(CT857)	CT857 Hypothetical Protein	0012	0209	0460	1040
1016	(CT858)	CT858 Hypothetical Protein	0028	0210	0461	1051
1019	(CT860)	CT860 Hypothetical Protein	0029	0211	0462	1052
1020	(CT861)	CT861 Hypothetical Protein	0034	0212	0463	1053
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1032	(CT373)	CT373 Hypothetical Protein	0042	0214	0465	1055
1033	(CT372)	CT372 Hypothetical Protein	0043	0215	0472	1056
1034	(CT371)	CT371 Hypothetical Protein	0044	0216	0473	1064
1057	(CT356)	CT356 Hypothetical Protein	0045	0218	0481	1065
1058	(CT355)	CT355 Hypothetical Protein	0046	0220	0483	1066
1061	(CT330)	CT330 Hypothetical Protein	0047	0221	0492	1070
1073	(CT371)	CT371 Hypothetical Protein	0049	0222	0493	1071
Coding Genes Not in <i>C. trachomatis</i>				0050	0223	0494
0486		Hypothetical Proline Permease	0051	0224	0498	
0279		Possible ABC Transporter Permease Protein	0063	0225	0499	
0505		3-Methyladenine DNA Glycosylase	0064	0226	0516	
0193	argR	Similarity to Arginine Repressor	0066	0233	0517	
1041	bioA	Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase	0067	0240	0523	
1044	bioB	Biotin Synthase	0069	0241	0524	
1042	bioD	Dethiobiotin synthetase	0070	0242	0553	
0585		Similarity to Cps IncA_2	0099	0243	0574	
0562		CHLPS 43 kDa Protein Homolog_1	0124	0266	0600	
0927		CHLPS 43 kDa Protein Homolog_2	0125	0267	0656	
0928		CHLPS 43 kDa Protein Homolog_3	0126	0268	0664	
0929		CHLPS 43 kDa Protein Homolog_4	0130	0277	0677	
1045		Conserved Hypothetical Membrane Protein	0131	0283	0678	
0251		Conserved Hypothetical Protein	0132	0284	0685	
0278		Conserved Outer Membrane Lipoprotein Protein	0142	0285	0686	
0907		CutA-like Periplasmic Divalent Cation Tolerance Protein	0146	0287	0724	
0171	guaA	GMP Synthase	0147	0352	0731	
0172	guaB	Inosine 5'-Monophosphate Dehydrogenase	0155	0353	0745	
0608		Uridine 5'-Monophosphate Synthase	0156	0354	0753	
0735		Uridine Kinase	0157	0355	0794	
0980		Similar to <i>Saccharomyces cerevisiae</i> 52.9kDa Protein	0158	0356	0795	
0232		Similarity to 5'-Methylthioadenosine Nucleosidase	0159	0357	0796	
1046		Tryptophan Hydroxylase	0162	0358	0797	
0477	yqeV_Bs	Conserved Hypothetical Protein	0164	0366	0798	
0048	yqfF_Bs	Conserved Hypothetical IM Protein	0165	0367	0829	
0587	yyvD_Bs	Conserved Hypothetical Protein	0166	0368	0830	
0143	yxjG_Bs_1	Conserved Hypothetical Protein	0167	0371	0831	
0448	yxjG_Bs_2	Conserved Hypothetical Protein	0168	0372	0881	
0006	0180	0440 0977	0169	0375	0882	
0007	0181	0455 0978	0170	0376	0913	
0008	0190	0456 1018	0173	0391	0914	
0009	0203	0457 1023	0174	0398	0930	
0010	0204	0458 1027	0175	0404	0944	
			0177	0431	0964	
			0178	0432	0975	
			0179	0439	0976	

The image shows a screenshot of the NCBI Protein search interface. At the top, there's a navigation bar with links to Entrez, PubMed, Nucleotide, Protein, Genome, Structure, PMC, Taxonomy, and Books. Below the navigation bar is a search bar with the word "Protein" and a dropdown menu set to "Search". There are also buttons for "Search", "View", and "Print". Below the search bar are buttons for "Limits", "Previous/Index", "History", "Clipboard", and "Details". A message "You need JavaScript to work with this page." is displayed. Below these controls is a table with columns for "default", "Show:", and "File".

1: [P38001. 50S ribosomal pro...\[gi:7404434\]](#) [BLink](#), [Domains](#), [Links](#)

LOCUS P38001 130 aa linear BCT 01-OCT-2004
DEFINITION 50S ribosomal protein L7/L12.
ACCESSION P38001
VERSION P38001 GI:7404434
DBSOURCE swissprot: locus RL7_CHLMU, accession P38001;
class: standard.
created: Oct 1, 1994.
sequence updated: May 30, 2000.
annotation updated: Oct 1, 2004.
xrefs: gi: 8163261, gi: 7190628, gi: 11276725
xrefs (non-sequence databases): HSSPP02392, Siena-2DPAGEP38001,
TIGRTC0590, HAMAPMF_00368, InterProIPR000206, InterProIPR008932,
PfamPF00542, ProDomPD001326, TIGRFAMsTIGR00855
KEYWORDS Complete proteome; Ribosomal protein.
SOURCE Chlamydia muridarum
ORGANISM [Chlamydia muridarum](#)
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE 1 (residues 1 to 130)
AUTHORS Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
White,O., Hickey,E.K., Peterson,J., Utterback,T., Berry,K.,
Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B., Bowman,C.,
Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J., McClarty,G.,
Salzberg,S.L., Eisen,J. and Fraser,C.M.
TITLE Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39
JOURNAL Nucleic Acids Res. 28 (6), 1397-1406 (2000)
MEDLINE 20150255
PUBMED 10684935
REMARK SEQUENCE FROM N.A.
STRAIN=MoPn / Nigg
REFERENCE 2 (residues 1 to 130)
AUTHORS Engel,J.N., Pollack,J., Malik,F. and Ganem,D.
TITLE Cloning and characterization of RNA polymerase core subunits of
Chlamydia trachomatis by using the polymerase chain reaction
JOURNAL J. Bacteriol. 172 (10), 5732-5741 (1990)
MEDLINE 91008945
PUBMED 2211507
REMARK SEQUENCE OF 2-127 FROM N.A.
STRAIN=MoPn
COMMENT On Apr 3, 2000 this sequence version replaced gi:585891.

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The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[FUNCTION] Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).

[SIMILARITY] Belongs to the L12P family of ribosomal proteins.

FEATURES Location/Qualifiers

source 1..130
/organism="Chlamydia muridarum"
/db_xref="taxon:83560"

gene 1..130
/gene="rplL"
/locus_tag="TC0590"

Protein 1..130
/gene="rplL"
/locus_tag="TC0590"
/product="50S ribosomal protein L7/L12"

Region 15
/gene="rplL"
/locus_tag="TC0590"
/region_name="Conflict"
/note="G -> R (in Ref. 2)."

Region 52
/gene="rplL"
/locus_tag="TC0590"
/region_name="Conflict"
/note="A -> R (in Ref. 2)."

Region 60..128
/gene="rplL"
/locus_tag="TC0590"
/region_name="Ribosomal protein L7/L12 C-terminal domain"
/note="Ribosomal_L12"
/db_xref="CDD:1101"

ORIGIN

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61 faviledvpa dkkigvlkvv revtglalke akemteglpk tvkektsksd aedtvkklqe
121 agakavakgl

//